PARAMETER ESTIMATION IN NON-CLOSED SOCIAL NETWORKS RELATED TO DYNAMICS OF SEXUALLY TRANSMITTED DISEASES

Shu-Fang HSU SCHMITZ[†]
Carlos CASTILLO-CHAVEZ*

Current address for both authors:
Biometrics Unit
337 Warren Hall
Cornell University
Ithaca, NY 14853-7801
Tel: (607) 255-5488
Fax: (607) 255-4698

[†]Address after Oct. 31, 1993:
Inst. f. math. Statistik
Universität Bern
Sidlerstr. 5
CH-3012 Bern
Switzerland

* To whom proofs should be sent.

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1. Introduction

The process of defining, modeling, and estimating parameters useful for the study of dynamic contact structures is of great importance to such fields as social dynamics, epidemiology, population genetics, cultural anthropology, demography, evolutionary biology, ecology and immunology. For example, age-dependent contact structures have been used in the study of the dynamics of communicable diseases (CD's) and mathematical epidemiology since 1974 (see (1)–(7)). CD's such as measles, chicken pox, influenza, and colds are transmitted mostly through casual contacts. Mathematical models help one understand and quantify the effects that age-dependent contact structures have on the transmission dynamics of CD's. Outbreaks usually begin in schools where the rate of casual contacts is higher than in other social settings. The high level of contacts between children has been used to explain primary and secondary outbreaks of some CD's (see (4)).

Casual contacts, the main mode of transmission of CD's, are adequately modeled through the use of proportionate mixing, in which all individuals are assigned age-dependent activity levels and where contacts are assumed to occur in proportion to age-dependent activity levels weighted by their corresponding density (see (8), (9)). On average, children may have more contacts because they are more active and/or because they represent a larger proportion of the age-structured population.

The contact structure is not the only feature of importance in the study of the transmission dynamics of CD's; for example, time scales may be quite relevant (see (5), (6)). In many instances, there is a significant difference between a host's life expectancy and the average length of the disease's infectious period. To study single episodic events it is common to ignore demographic effects by assuming that the population under consideration has reached a stable age distribution. This last assumption may also be useful in the study of the long-term dynamics of CD's where disease-induced mortality is not a factor and where the rate of population growth is not significant. The use of proportionate mixing and the assumption that a population has reached a stable age distribution have been quite useful in the study of disease persistence (endemicity), in the evaluation of disease control strategies, and in the study of the effectiveness of vaccination programs (see (3), (7), (10)). The

usefulness of these assumptions in today's world is becoming limited for modeling of treatable and untreatable sexually transmitted diseases (STD's) due to large increases in migration and travel rates within and between populations.

Proportionate mixing provides an appropriate model of population heterogeneity in the context of CD dynamics but does not provide an all purpose model. Epidemiological data, biological and sociological realism, and important demographic considerations did not play an important role (with some exceptions, see (11)–(16)) in the development of mathematical and theoretical epidemiology until the dramatic rise of HIV and AIDS. The spread of HIV/AIDS, particularly in industrialized nations, forced theoreticians to examine potential mechanisms for the spread of HIV using more plausible scenarios. Realistic models incorporating the role of long and variable incubation periods, age-of-infection infectivity, and social dynamics have been developed by a large number of researchers (see (17)–(27)). The importance of social dynamics, the main topic of this chapter, emerged with the generation of models that incorporate relevant sociological/epidemiological factors including varying degrees of sexual activity, alternate modes of transmission (needle sharing, anal sex, etc.), sexual preference (bi-, hetero-, and homo-sexual activity), and heterogeneity in pairing/contact structures (see (8), (9), (28)–(50)).

Research on statistical and mathematical approaches to HIV dynamics has been extensive over the last seven years. Several volumes devoted to issues of importance to HIV/AIDS dynamics including parameter estimation, short-term predictions, forecasting, social dynamics, and immunology have appeared over the last several years (see (19), (51), (52)). The recent book by Hethcote and Van Ark (53) provides a detailed data-driven study of HIV dynamics, while the encyclopedic book by Anderson and May (7) gives a panoramic view of the growing field of theoretical epidemiology with emphasis on the extensive contributions of Anderson, May, and their collaborators.

While the contact structure of a population is one of the main factors influencing the incidence of sexually-transmitted diseases, it has been proven difficult to determine population mixing patterns from observable data. Even in situations where reasonable samples have been drawn from selected target populations (such as college students, bar patrons, or participants in drug treatment programs),

members of the target group interact significantly with members *outside* the target group. This latter situation is problematic for existing models which implicitly assume that the populations are *closed*, that is, all social or sexual contacts occur within the groups specified in the model. To enable such models to be employed, a procedure is needed to "close" the population on the basis of incomplete observations.

This paper proposes a new approach to the estimation of non-random contact patterns that explicitly recognizes the interaction between members of a target population (who *can* be sampled) and individuals in non-target populations (who *cannot* be sampled). Included in our contribution is a method for estimating the size of the non-target population that is interacting with the target population sampled. This allows us to construct a pattern of interactions among target and non-target populations that is consistent with known axioms of population mixing. Our technical work developed alongside our empirical study of dating and sexual activity among college students (see (54)-(57)). This survey reveals that random mating is not descriptively accurate, and highlights convincingly the strength of the social or sexual interaction between the target and non-target populations. While our study may not be representative of all U.S. college students, the features we infer from our sample via our modeling approach are in line with our daily unscientific observations (e.g., strong within class mixing, women prefer to mix with older men). The development of a methodology that incorporates these features into models of STD transmission dynamics is the goal of this chapter.

We proceed as follows: Section 2 describes a general axiomatic approach for modeling contact processes in heterogeneous mixing populations, while Section 3 employs this framework to model dating, sexual mixing, and pair-formation in the context of heterosexually active populations. The data structure used to illustrate our approach to constructing mixing matrices is described in Section 4. In Section 5, we present a mark-recapture model for estimating the size of the non-target population that interacts with our sampled target population. Section 6 reduces the problem of completely specifying mixing matrices to that of estimating a single parameter. Our completion algorithm is illustrated in Section 7 using the data from our survey of college undergraduates. Section 8 summarizes our results and discusses potential applications of the algorithm.

2. Mixing between I interacting subpopulations

Busenberg and Castillo-Chavez (see (8), (9)) have shown that all mixing structures where individuals interact with members of all subpopulations can be expressed as a multiplicative perturbation of proportionate mixing. In this section we briefly summarize their result using a population comprising I distinct types or groups. The ith group has $T_i(t)$ individuals at time t and an average number of C_i partners per person per unit time. The social/sexual contact structure of the population is modeled by an $I \times I$ matrix of probabilities $P(t)$, where $P_{ij}(t)$ gives the probability that a partner selected by a sexually active individual at time t in group i is a member of group j. The matrix $P(t)$ must satisfy the following constraints or mixing axioms:

(A1) $P_{ij}(t) \geq 0$ for $1 \leq i, j \leq I$ and all t.

(A2) $\sum_{j=1}^{I} P_{ij}(t) = 1$ for $1 \leq i \leq I$ and all t.

(A3) $C_i\, T_i(t)\, P_{ij}(t) = C_j\, T_j(t)\, P_{ji}(t)$ for $1 \leq i, j \leq I$ and all t.

Constraints (A1) and (A2) make P a stochastic matrix while (A3) guarantees conservation in the number of new pairings/contacts per unit time between types. Busenberg and Castillo-Chavez's representation theorem states that *any* P that satisfies the constraints (A1)–(A3) may be written in the form:

$$P_{ij} = \overline{P}_j \left[\frac{Q_i\, Q_j}{V} + \phi_{ij} \right] \quad \text{for } 1 \leq i, j \leq I; \tag{1}$$

where

$$\overline{P}_j = \frac{C_j\, T_j}{\sum_{k=1}^{I} C_k\, T_k} \quad \text{for } 1 \leq j \leq I \tag{2}$$

represents random or proportionate mixing between groups,

$$Q_i = 1 - \sum_{k=1}^{I} \overline{P}_k\, \phi_{ik} \quad \text{for } 1 \leq i \leq I, \tag{3}$$

$$V = \sum_{k=1}^{I} \overline{P}_k\, Q_k\,, \tag{4}$$

and $\phi = \{\phi_{ij}\}$ is an $I \times I$ symmetric matrix. The matrix ϕ is a measure of *mutual preference* or *affinity* for sexual partners between pairs of groups (see (33), (36), (58)–(60)). Specific preference structures are determined by the elements of the ϕ matrix. For example, following Blythe and Castillo-Chavez (61)

we may parametrize ϕ as follows:

(i) Each ϕ_{ij} can take one of only two values, a or b, where $0 \leq b \leq a < 1$.

(ii) All the elements in each diagonal or off-diagonal of the ϕ matrix are the same; for example, for I=4, the ϕ matrices may look like:

$$\phi = \begin{bmatrix} a & b & b & b \\ b & a & b & b \\ b & b & a & b \\ b & b & b & a \end{bmatrix} \quad \text{or} \quad \phi = \begin{bmatrix} a & a & b & b \\ a & a & a & b \\ b & a & a & a \\ b & b & a & a \end{bmatrix}.$$

This restriction on the mixing parameters $\{\phi_{ij}\}$ gives us a mixing framework (the function on the RHS of Equation (1)) that is fairly simple (only two values are used to describe the ϕ matrix) and capable of considerable flexibility. We note that if a=b we recover proportionate mixing, while a flexible form of like-with-like mixing is obtained with the parametrization ϕ_{ij}=a if i=j, ϕ_{ij}=b otherwise.

Multigroup models for STD's have been studied by a variety of groups including Lajmanovich and Yorke (62), Jacquez *et al.* (45), Castillo-Chavez *et al.* (22), Huang *et al.* (25), and Huang (63). Many researchers have been satisfied with the use of proportionate mixing (Equation (2)) or preferred mixing because of their mathematical simplicity (but see (22), (25), and (63)). Since our main objective in this chapter is to present our method for determining the shape of the mixing matrix, it is important to keep in mind as reference models the shapes of proportionate mixing and of preferred mixing. The latter one is given by

$$P_{ij} = h_i \, \delta_{ij} + (1 - h_i) \frac{(1 - h_j) \, \overline{P}_j}{\sum_{k=1}^{I} (1 - h_k) \, \overline{P}_k} \quad , \tag{5}$$

where the h_i's are non-negative constants between zero and one. These constants represent the proportions of group contacts/partnerships that are "reserved" for within-group mixing. The term δ_{ij} equals 1 if i=j and 0 otherwise. Consequently, those partnerships that are not reserved for within-group mixing are assumed to follow proportionate mixing. Figure 1 illustrates the shape of a random or proportionate mixing matrix (h_i=0 for all i) obtained from the aggregated data presented in Section

7 with pair-formation parameter=2. Figure 2 shows a preferred mixing matrix with h_i=0.2 for all i, a "diagonal" perturbation from Figure 1. Another perturbation is presented in Figure 3, using h_1=h_5=0.4, h_2=h_4=0.3, and h_3=0.2. Preferred mixing, as shown by Blythe and Castillo-Chavez (64), corresponds to the (frequency dependent) preference function $\phi_{ij}=h_i\delta_{ij}/\overline{P}_i$. Thus, to maintain a fixed proportion of contacts with one's group regardless of the population dynamics, individuals must continually adjust their preference. This again highlights the deficiencies of this model.

Finally, because the data collected come from two-sex sexual or dating interactions, we are forced to modify the framework of this section to include this added social structure. This is the topic of the next section in this chapter.

3. Two-sex mixing structures

In this section, we introduce two-sex mixing structures in a heterosexually active population with $(I+J)$ groups. The notation is similar to that in Section 2, except that we use superscripts m and f, and subscripts i and j for males and females, respectively. This population is divided into groups or subpopulations which are defined by gender and possibly, race, socio-economic background, average degree of sexual activity, etc. We consider I sexually active groups of males and J sexually active groups of females. The following definitions are needed:

$P_{ij}^m(t)$: fraction of partnerships of males in group i with females in group j at time t,

$P_{ji}^f(t)$: fraction of partnerships of females in group j with males in group i at time t,

C_i^m : average (constant) number of female partners per male in group i per unit time, or the pair-formation rate of ith male group,

C_j^f : average (constant) number of male partners per female in group j per unit time, or the pair-formation rate of jth female group,

The set of mixing probabilities $\{P_{ij}^m(t)$ and $P_{ji}^f(t)$: i=1, ..., I and j=1, ..., $J\}$ establishes the mixing/pair-formation structure in heterosexually active populations provided they satisfy the following definition.

Def $\{P_{ij}^m(t),\ P_{ji}^f(t)\}$ is called a mixing/pair-formation matrix if and only if it satisfies the following properties at all times:

(B1) $0 \le P_{ij}^m(t) \le 1$ and $0 \le P_{ji}^f(t) \le 1$ for $i=1, \ldots, I,\ j=1, \ldots, J$ and all t.

(B2) $\sum_{j=1}^{J} P_{ij}^m(t) = 1$ for $i=1, \ldots, I$ and all t; $\sum_{i=1}^{I} P_{ji}^f(t) = 1$ for $j=1, \ldots, J$ and all t.

(B3) $C_i^m\ T_i^m(t)\ P_{ij}^m(t) = C_j^f\ T_j^f(t)\ P_{ji}^f(t)$ for $i=1, \ldots, I,\ j=1, \ldots, J$ and all t.

Property (B3) can be interpreted as a conservation of partnership-formation rates between two groups. A useful particular solution is the Ross solution which corresponds to proportionate mixing in the context of heterosexually active populations. The Ross solution is denoted by $\{\overline{P}_i^m, \overline{P}_j^f\}$, where

$$\overline{P}_j^m = \frac{C_j^f\ T_j^f}{\sum_{i=1}^{I} C_i^m\ T_i^m} \quad \text{and} \quad \overline{P}_i^f = \frac{C_i^m\ T_i^m}{\sum_{j=1}^{J} C_j^f\ T_j^f} \tag{6}$$

for $j=1, \ldots, J$ and $i=1, \ldots, I$. Note that $\sum_{i=1}^{I} C_i^m T_i^m(t) = \sum_{j=1}^{J} C_j^f\ T_j^f(t)$ at all time by (B3). All solutions to axioms (B1)–(B3) can be generated as multiplicative perturbations of the Ross solution. Figures 4 and 5 illustrate the shape of feasible male and female random mixing matrices generated from our survey data under the assumption of heterosexual random mixing. The real mixing matrices for the first four groups, using the same pair-formation parameter, are sketched in Figures 6 and 7. It is clear that this sample from the target population does not mix at random. To describe nonrandom mixing in mathematical terms, that is, all perturbations of the Ross solution satisfying (B1)-(B3), we need the following definitions:

ϕ_{ij}^m = measure of preference that group i males have for group j females,

$i=1, \ldots, I$ and $j=1, \ldots, J$;

$\ell_i^m = \sum_{k=1}^{J} \overline{P}_k^m\ \phi_{ik}^m$ = weighted average preference of group i males, $i=1, \ldots, I$;

$Q_i^m = 1 - \ell_i^m$, $i=1, \ldots, I$.

We require at all times that $0 \le Q_i^m \le 1$ and that

$$\sum_{i=1}^{I} \ell_i^m\ \overline{P}_i^f = \sum_{i=1}^{I} \sum_{k=1}^{J} \overline{P}_k^m\ \phi_{ik}^m\ \overline{P}_i^f < 1\ . \tag{7}$$

Similarly, we let

ϕ^f_{ji} = measure of preference that group j females have for group i males,

$j=1, \ldots, J$ and $i=1, \ldots, I$;

$\ell^f_j = \sum_{l=1}^{I} \overline{P}^f_l \, \phi^f_{jl}$ = weighted average preference of group j females, $j=1, \ldots, J$;

$Q^f_j = 1 - \ell^f_j$, $j=1, \ldots, J$.

Again, we require at all times that $0 \leq Q^f_j \leq 1$ and that

$$\sum_{j=1}^{J} \ell^f_j \, \overline{P}^m_j = \sum_{j=1}^{J} \sum_{l=1}^{I} \overline{P}^f_l \, \phi^f_{jl} \, \overline{P}^m_j < 1 \, . \tag{8}$$

Using the above notation, Castillo-Chavez and Busenberg (35) have shown that all solutions to axioms (B1)–(B3) are given by the following multiplicative perturbations to the Ross solution $\{\overline{P}^m_j, \overline{P}^f_i\}$:

$$P^m_{ij} = \overline{P}^m_j \left[\frac{Q^f_j \, Q^m_i}{\sum_{l=1}^{I} \overline{P}^f_l \, Q^m_l} + \phi^m_{ij} \right] \quad \text{and} \quad P^f_{ji} = \overline{P}^f_i \left[\frac{Q^m_i \, Q^f_j}{\sum_{k=1}^{J} \overline{P}^m_k \, Q^f_k} + \phi^f_{ji} \right] \tag{9}$$

for $i=1, \ldots, I$, $j=1, \ldots, J$. Their theorem explicitly states:

Theorem Let $\{\phi^m_{ij}\}$ and $\{\phi^f_{ji}\}$ be two nonnegative matrices. Let $\ell^m_i = \sum_{k=1}^{J} \overline{P}^m_k \phi^m_{ik}$ and $\ell^f_j = \sum_{l=1}^{I} \overline{P}^f_l \phi^f_{jl}$, where $\{\overline{P}^m_j, \overline{P}^f_i$: $j=1, \ldots, J$ and $i=1, \ldots, I\}$ denotes the Ross solution. Let $Q^m_i = 1 - \ell^m_i$, $i=1, \ldots, I$ and $Q^f_j = 1 - \ell^f_j$, $j=1, \ldots, J$. If ϕ^m_{ij} and ϕ^f_{ji} are chosen in such a way that $0 \leq Q^m_i \leq 1$, $0 \leq Q^f_j \leq 1$, $\sum_{i=1}^{I} \ell^m_i \, \overline{P}^f_i < 1$, and $\sum_{j=1}^{J} \ell^f_j \, \overline{P}^m_j < 1$,

then

$$\phi^m_{ij} = \phi^f_{ji} + Q^m_i \, Q^f_j \left[\frac{\sum_{k=1}^{J} \overline{P}^m_k \, Q^f_k - \sum_{l=1}^{I} \overline{P}^f_l \, Q^m_l}{\left(\sum_{l=1}^{I} \overline{P}^f_l \, Q^m_l \right) \left(\sum_{k=1}^{J} \overline{P}^m_k \, Q^f_k \right)} \right] \tag{10}$$

if and only if all solutions to axioms (B1)–(B3) are given by (9).

Although the above representation theorem looks rather complicated, we can easily use it to generate a large number of solutions with only one or two parameters. It is possible to generate the type of mixing observed in the data used in Sections 4–7 to test our algorithm because Hsu Schmitz *et*

al. (65) have shown that all parametrizations for $\{\phi_{ij}^m\} = \{\phi_{ji}^f\}^T$ are legitimate (*i.e.*, they satisfy all the conditions of the above theorem including Equation (10)). This result immediately allows the generation of a rich and flexible class of parametric solutions. However, we will not pursue this direction in this chapter.

4. Data structure of non-closed networks

The mixing structures discussed in Section 2 and Section 3 are applicable to closed populations by the implicit assumption that all population groups are captured in the model. For data collected from the real world, the population covered is probably not closed. Usually the data cover not only the target population but also the non-target population. If the non-target population plays a considerable role in the network, then we should not ignore it. Without direct information on the non-target population, the mixing matrices are not complete, and demographic dynamics and disease transmission can not be predicted correctly. Therefore, the issue of how to obtain indirect information on the non-target populations and their effect on network interactions must be addressed prior to further study. In this section, we describe the potential data structure of non-closed two-sex mixing populations. Then we conditionally "close" the network and complete the mixing matrices in Sections 5 and 6. An illustrative example is provided in Section 7.

Following the notation in Section 3, we let the Ith male group and the Jth female group consist of individuals from the non-target populations (that is, they are members of an unobservable subpopulation). The first I–1 male groups and the first J–1 female groups are composed of males and females from the target populations, respectively. Suppose we are interested in the heterosexual contact structure of a given target population at a given time and we know the sizes of the target male groups, R_i^m (i=1, $\cdots$, I–1), and of the target female groups, R_j^f (j=1, $\cdots$, J–1). To gather data for this study, we do stratified sampling at a given time to randomly select respondents from those I–1 male groups and those J–1 female groups to our questionnaire. The questions concerning a given time period (our time unit) are: if they were sexually active or not; if yes, how many distinct partners they had; and how many of those partners belonged to different target and non-target groups. In our data

the term *sexually active* means having sexual contacts during the given time period. The data are represented by the following notation:

S_i^m : sample size of ith target male group, i=1, ···, I–1;

S_j^f : sample size of jth target female group, j=1, ···, J–1;

A_i^m : number of *sexually active* individuals among S_i^m;

A_j^f : number of *sexually active* individuals among S_j^f;

Y_{ik}^m : number of distinct female partners of individual k in A_i^m;

Y_{jr}^f : number of distinct male partners of individual r in A_j^f;

X_{ik}^m : among Y_{ik}^m , number of distinct female partners from the target population;

X_{jr}^f : among Y_{jr}^f , number of distinct male partners from the target population;

U_{ijk}^m : among Y_{ik}^m , number of distinct female partners from group j;

U_{jir}^f : among Y_{jr}^f , number of distinct male partners from group i.

We can summarize the data by

$$Y_{i\cdot}^m = \sum_{k=1}^{A_i^m} Y_{ik}^m = \text{total number of female partners of individuals in } A_i^m ;$$

$$Y_{j\cdot}^f = \sum_{r=1}^{A_j^f} Y_{jr}^f = \text{total number of male partners of individuals in } A_j^f ;$$

$$X_{i\cdot}^m = \sum_{k=1}^{A_i^m} X_{ik}^m = \text{among } Y_{i\cdot}^m \text{ , total number of female partners from the target population;}$$

$$X_{j\cdot}^f = \sum_{r=1}^{A_j^f} X_{jr}^f = \text{among } Y_{j\cdot}^f \text{ , total number of male partners from the target population;}$$

$$Y_+^m = \sum_{i=1}^{I-1} Y_{i\cdot}^m = \text{total number of female partners of all sampled } \textit{sexually active} \text{ males;}$$

$$Y_+^f = \sum_{j=1}^{J-1} Y_{j\cdot}^f = \text{total number of male partners of all sampled } \textit{sexually active} \text{ females;}$$

$$X_+^m = \sum_{i=1}^{I-1} X_{i\cdot}^m = \text{among } Y_+^m \text{ , total number of female partners from the target population;}$$

$$X_+^f = \sum_{j=1}^{J-1} X_{j\cdot}^f = \text{among } Y_+^f \text{ , total number of male partners from the target population;}$$

$$U^m_{ij.} = \sum_{k=1}^{A^m_i} U^m_{ijk} = \text{among } Y^m_{i.}\text{, total number of female partners from group } j;$$

$$U^f_{ji.} = \sum_{r=1}^{A^f_j} U^f_{jir} = \text{among } Y^f_{j.}\text{, total number of male partners from group } i.$$

We can obtain point estimates of the average number of partners per person per unit time and of the entries in the mixing matrix as follows:

$C^m_i = Y^m_{i.}/A^m_i$ = average number of female partners per *sexually active* male in group i per unit time, i=1, ···, I–1;

$C^f_j = Y^f_{j.}/A^f_j$ = average number of male partners per *sexually active* female in group j per unit time, j=1, ···, J–1;

$P^m_{ij} = U^m_{ij.}/Y^m_{i.}$ = fraction of sexual contacts of males in group i with females in group j at the given time, i=1, ···, I–1 and j=1, ···, J;

$P^f_{ji} = U^f_{ji.}/Y^f_{j.}$ = fraction of sexual contacts of females in group j with males in group i at the given time, j=1, ···, J–1 and i=1, ···, I.

The matrix, $\{P^m_{ij}, P^f_{ji}\}$, from the above data structure is not complete because we do not have a closed network: individuals in the non-target male and female populations were not surveyed, so the rows $\{P^m_{Ij}\}$ and $\{P^f_{Ji}\}$ are missing. Sections 5 and 6 show how to conditionally "close" the network and complete this matrix but do not guarantee that $U^m_{ij.} = U^f_{ji.}$ as required by theory. The problem arises from the fact that we are dealing with a sample and not a census (this is evident in Tables 2 and 3). Usually data satisfy axioms (B1) and possibly (B2) but not axiom (B3). The same is true for estimates of $\{P^m_{Ij}\}$ and $\{P^f_{Ji}\}$.

5. Mark-recapture methodology for estimating non-target population sizes

We assume that the group sizes in the target population are known. However, the sizes of the *sexually active* subgroups, T^g_v (g=m or f, v=1, ···, I–1 or J–1), are not known. The assumption that all individuals in these groups were *sexually active* is certainly not realistic. A natural way to estimate the *sexually active* group sizes is given by the following formulas:

$$\hat{T}_i^m = R_i^m \times (A_i^m / S_i^m) \quad \text{and} \quad \hat{T}_j^f = R_j^f \times (A_j^f / S_j^f) \,, \tag{11}$$

where R_i^m and R_j^f denote the known target group sizes, i=1, ···, I–1 and j=1, ···, J–1. In fact, these estimators are the maximum likelihood estimators (see (55)). Because the survey's definition of *sexually active* is tied up with a specific time period (a very narrow definition), individuals in the target population who are sexually active but did not have sexual contacts during that specific period do not contribute to the above estimates. Since we do not have direct information on the non-target male and female populations, the sizes of their *sexually active* subsets have to be estimated by other methods. Rubin *et al.* (55) introduced modified mark-recapture methods to obtain conditional estimates of the sizes of these subsets. The general procedure is summarized in two steps below.

First mark a random sample of size n_1 from a population of size N (unknown) and release them. After a certain period of time, the second step which collects a random sample of size n_2 from the same population is enforced. The number of marked individuals in this second sample is denoted by m_2. Bailey (66) introduced the binomial model as a useful approximation to the classic hypergeometric model that arises when only a single capture is possible after marking. His model is given by the expression

$$\mathrm{P}(m_2 | n_1, n_2) \approx \binom{n_2}{m_2} \left(\frac{n_1}{N}\right)^{m_2} \left(1 - \frac{n_1}{N}\right)^{n_2 - m_2} . \tag{12}$$

If individuals are sighted by observers, instead of physically captured, then since different observers may sight the same individuals, individuals in the population may be sampled with replacement. If sampling is done with replacement, then the binomial model holds exactly (see (67)). Because the maximum likelihood estimator for N, namely $N^* = n_1 n_2 / m_2$ (the Lincoln-Petersen estimator), is biased, Bailey (66) suggested the following estimator for N, $\hat{N}$, and for its variance, $\hat{v}(\hat{N})$:

$$\hat{N} = \frac{n_1 \, (n_2 + 1)}{m_2 + 1} \,, \tag{13}$$

$$\hat{v}(\hat{N}) = \frac{(n_1)^2 \, (n_2 + 1) \, (n_2 - m_2)}{(m_2 + 1)^2 \, (m_2 + 2)} \,. \tag{14}$$

These estimators are less biased with proportional biases of order $\exp(-n_1 n_2 / N)$ and

$(n_1 n_2/N)^2 \exp(-n_1 n_2/N)$, respectively. For the data structure described in Section 4, we assume that all *sexually active* individuals of a given gender g in the target population are marked and those in the sample constitute the first sample of size T_+^g. Individuals sampled who were *sexually active* serve as observers who "sight" their partners of the other gender by sexual/social contact. Thus, those partners from the target (marked) and non-target (unmarked) populations constitute the second sample. Because different observers may have the same sexual partners, the second sampling procedure for partners must be done with replacement. Bailey's binomial model is exact in this case and hence more appropriate for our data. By Equation (13), the estimates of the total number of *sexually active* individuals in the target and non-target populations for both genders are

$$\hat{N}^m = \frac{T_+^m\,(Y_+^f + 1)}{X_+^f + 1} \quad \text{and} \quad \hat{N}^f = \frac{T_+^f\,(Y_+^m + 1)}{X_+^m + 1}. \tag{15}$$

Note that the information in the second sample is from observers of the other gender. The estimated variances of $\hat{N}^m$ and $\hat{N}^f$ are analogous to those in Equation (14). However, T_+^m and T_+^f are not known in our case. We estimate them as

$$\hat{T}_+^m = \sum_{i=1}^{I-1} \hat{T}_i^m \quad \text{and} \quad \hat{T}_+^f = \sum_{j=1}^{J-1} \hat{T}_j^f\,; \tag{16}$$

and use these estimates to obtain the maximum likelihood estimates of the total number of *sexually active* individuals, $\tilde{N}^g$:

$$\tilde{N}^m = \frac{\hat{T}_+^m\,(Y_+^f + 1)}{X_+^f + 1} \quad \text{and} \quad \tilde{N}^f = \frac{\hat{T}_+^f\,(Y_+^m + 1)}{X_+^m + 1}. \tag{17}$$

The estimated variances of $\tilde{N}^m$ and $\tilde{N}^f$ are provided by Rubin et al. (55). These variances incorporate the additional variation due to $\hat{T}_+^m$ and $\hat{T}_+^f$. Since $\tilde{N}^m$ and $\tilde{N}^f$ include *sexually active* individuals from the target and non-target populations, that is, $\tilde{N}^m = \hat{T}_+^m + \hat{T}_I^m$ and $\tilde{N}^f = \hat{T}_+^f + \hat{T}_J^f$, the estimated sizes of *sexually active* non-target populations are

$$\hat{T}_I^m = \tilde{N}^m - \hat{T}_+^m = \frac{\hat{T}_+^m\,(Y_+^f - X_+^f)}{X_+^f + 1} \quad \text{and} \quad \hat{T}_J^f = \tilde{N}^f - \hat{T}_+^f = \frac{\hat{T}_+^f\,(Y_+^m - X_+^m)}{X_+^m + 1}. \tag{18}$$

However, *sexually active* individuals in the non-target population will not be "sighted" if they did not engage in sexual activity with individuals from the target population. Therefore, $\hat{T}_I^m$ and $\hat{T}_J^f$ are

conditional estimates which count only those individuals in the non-target population who had at least one sexual contact with partners from the target population of the opposite gender during the surveyed period. This is one of the first data sets of this type, and its limitations may be perceived as too strong. However, this data structure brings to the forefront the even stronger limitations that are implicit in current mathematical and statistical models.

We also observe that equations in (15) and (17) imply that individuals with high contact rates are more likely to be "sighted". It is nearly impossible to modify the sampling procedure to take into account this effect. An alternative approach is to modify these equations to incorporate the effects of the biases. Modifications should be closely connected to data and, consequently, to survey design. Our data, used in the example of Section 7, do not seem to be seriously affected by this source of biases as the "average" contact rates of the interacting subpopulations do not vary that much.

6. Completion of the mixing matrix

We assume that the combination of our target and non-target *sexually active* populations of both genders constitute a closed mixing network and hence its associated mixing matrix satisfies axioms (B1)–(B3). Using the mark-recapture methodology described in Section 5, we obtain conditional estimates for T_I^m and T_J^f. However, the rows $\{P_{Ij}^m\}$ and $\{P_{Ji}^f\}$, and the averages C_I^m and C_J^f are not yet known. We can obtain point estimates of these unknown parameters by assuming that the data are consistent with the above two-sex mixing framework, which reduces the estimation of all the unknown parameters to that of estimating a single pair-formation parameter. Then the shape of the complete mixing matrix can be calculated from the data. The procedure described in this section is an alternative version of that in (57).

First we sum over j on both sides of the equation in axiom (B3) and obtain

$$C_i^m \hat{T}_i^m = K_i^f + C_J^f \hat{T}_J^f P_{Ji}^f , \tag{19}$$

where $K_i^f = \sum_{j=1}^{J-1} C_j^f \hat{T}_j^f P_{ji}^f$ is non-negative (because C_j^f and $\hat{T}_j^f$ are positive, and P_{ji}^f are non-negative) and can be computed from the data (it is therefore known). Rearranging Equation (19) for $i=I$ yields

$$C_J^f \hat{T}_J^f P_{JI}^f = C_I^m \hat{T}_I^m - K_I^f \geq 0 , \tag{20}$$

which leads to a lower bound for C_I^m:

$$C_I^m \geq K_I^f \,/\, \hat{T}_I^m \,. \tag{21}$$

Similarly, we sum over i on both sides of the equation in axiom (B3) and obtain

$$C_j^f \; \hat{T}_j^f = K_j^m + C_I^m \; \hat{T}_I^m \; P_{Ij}^m \,, \tag{22}$$

where $K_j^m = \sum_{i=1}^{I-1} C_i^m \hat{T}_i^m P_{ij}^m$ is also known and non-negative. Rearranging Equation (22) for $j=J$ yields

$$C_I^m \; \hat{T}_I^m \; P_{IJ}^m = C_J^f \; \hat{T}_J^f - K_J^m \geq 0 \,, \tag{23}$$

which gives a lower bound for C_J^f:

$$C_J^f \geq K_J^m \,/\, \hat{T}_J^f \,. \tag{24}$$

Since only those sexually active individuals who had at least one sexual contact during the surveyed time period are under consideration, C_I^m and C_J^f must be greater than or equal to one. Therefore, we can use the following refined lower bounds

$$C_I^m \geq \max(K_I^f \,/\, \hat{T}_I^m \,,\; 1) \quad \text{and} \quad C_J^f \geq \max(K_J^m \,/\, \hat{T}_J^f \,,\; 1) \,. \tag{25}$$

To find the relationship between C_I^m and C_J^f, we sum over i and j on both sides of the equation in axiom (B3) and obtain

$$\sum_{i=1}^{I} C_i^m \; \hat{T}_i^m = \sum_{j=1}^{J} C_j^f \; \hat{T}_j^f \,, \tag{26}$$

or equivalently

$$C_I^m \; \hat{T}_I^m - C_J^f \; \hat{T}_J^f = G^f - G^m \,, \tag{27}$$

where $G^m = \sum_{i=1}^{I-1} C_i^m \; \hat{T}_i^m$ and $G^f = \sum_{j=1}^{J-1} C_j^f \; \hat{T}_j^f$, both can be computed from data.

Due to insufficient information in the data, there is no way of estimating unique values for C_I^m and C_J^f. But if one of these two parameters is known, then the other one can be uniquely obtained through Equation (27). In the absence of independent estimators for C_I^m or C_J^f, estimates of the rows $\{P_{Ij}^m\}$ and $\{P_{Ji}^f\}$ are not possible. Estimation of all the unknown parameters must be conditioned on the assumption that either C_I^m or C_J^f is known. If we assume that $\tilde{C}_I^m$ is an appropriate value for C_I^m, the pair-formation parameter, then

$$\tilde{C}_J^f = (\tilde{C}_I^m \; \hat{T}_I^m - G^f + G^m)/\hat{T}_J^f \,. \tag{28}$$

Plugging $\tilde{C}_I^m$ and $\tilde{C}_J^f$ into Equations (19) and (22) specifies the values of P_{Ji}^f and P_{Ij}^m, respectively:

$$\tilde{P}^f_{Ji} = \begin{cases} (C^m_i \ \hat{T}^m_i - K^f_i) \ / \ (\tilde{C}^f_J \ \hat{T}^f_J) & \text{for } i=1, \ldots, I-1, \\ (\tilde{C}^m_I \ \hat{T}^m_I - K^f_I) \ / \ (\tilde{C}^f_J \ \hat{T}^f_J) & \text{for } i=I. \end{cases} \tag{29}$$

$$\tilde{P}^m_{Ij} = \begin{cases} (C^f_j \ \hat{T}^f_j - K^m_j) \ / \ (\tilde{C}^m_I \ \hat{T}^m_I) & \text{for } j=1, \ldots, J-1, \\ (\tilde{C}^f_J \ \hat{T}^f_J - K^m_J) \ / \ (\tilde{C}^m_I \ \hat{T}^m_I) & \text{for } j=J. \end{cases} \tag{30}$$

By Equations (28), (29) and (30), the first derivatives of $\tilde{P}^m_{IJ}$ and $\tilde{P}^f_{JI}$ with respective to $\tilde{C}^m_I$ are:

$$\frac{\partial}{\partial \tilde{C}^m_I} \tilde{P}^m_{IJ} = \frac{G^f - G^m + K^m_J}{(\tilde{C}^m_I)^2 \ \hat{T}^m_I}, \tag{31}$$

$$\frac{\partial}{\partial \tilde{C}^m_I} \tilde{P}^f_{JI} = \frac{\hat{T}^m_I \ (G^m - G^f + K^f_I)}{(\tilde{C}^m_I \ \hat{T}^m_I - G^f + G^m)^2}. \tag{32}$$

Clearly the sign of $G^f - G^m + K^m_J$ determines if $\tilde{P}^m_{IJ}$ increases or decreases with $\tilde{C}^m_I$, and the sign of $G^m - G^f + K^f_I$ determines the behavior of $\tilde{P}^f_{JI}$. If $\tilde{P}^m_{IJ}$ increases with $\tilde{C}^m_I$, then some $\tilde{P}^m_{Ij}$ (j=1, ..., J-1) must decrease by axiom (B2). Similarly, if $\tilde{P}^f_{JI}$ increases with $\tilde{C}^m_I$, then some $\tilde{P}^f_{Ji}$ (i=1, ..., I-1) must decrease.

Thus, once we know the pair-formation parameter $\tilde{C}^m_I$, i.e., the average number of partners per male in the non-target population, we can obtain the average number of partners per female in the non-target population, $\tilde{C}^f_J$, and the mixing proportions for non-target populations, $\{P^m_{Ij}\}$ and $\{P^f_{Ji}\}$. The mixing matrix is now completed under the condition that all the *sexually active* individuals in the non-target populations have at least one sexual contact with individuals in the target populations.

Recall that we assume the combination of our target and non-target *sexually active* populations of both genders constitutes a closed network with a mixing matrix satisfying axioms (B1)–(B3). However, data collected from the real world may violate axioms (B3), and may result in estimated values of $\{P^m_{Ij}\}$ and $\{P^f_{Ji}\}$ that do not satisfy axioms (B1) or (B3). Since our main objective is to roughly determine the shape of the mixing matrix for a real population from a single sample, this violation is tolerated until a better method is developed.

7. Example

This example deals with the surveyed sexual behavior of college students as reported in (49)–(52). The target populations are male and female college students in a given university. Students of each gender are categorized by school year into four groups: 1 (freshman), 2 (sophomore), 3 (junior) and 4 (senior). In addition to these four groups, one more group, here referred as *other*, accounts for their partners who do not belong to the target population. The sizes of groups 1–4 for both genders are known since they are available from the university registrar's office.

Table 1 lists the group sizes (R), sample sizes (S), *sexually active* subsample sizes (A), *sexually active* proportions in the samples ($A \div S$), and estimated *sexually active* subgroup sizes ($\hat{T}$), all rounded to integers. Table 1 also includes the sums of the four groups in the target population. The observed overall *sexually active* proportion for male students is 34.1%, which is significantly smaller than the observed overall *sexually active* proportion 43.5% for female students (one-sided p=0.015). The sexual partnership distribution (U), the mixing proportions (P), the total (Y) and average (C) number of distinct partners for *sexually active* male and female students are presented in Table 2 and Table 3, respectively. Male students have a higher overall average number of distinct sexual partners (1.41) than female students (1.24); however, the difference is not significant (two-sided p=0.147). The overall proportion of sexual relationships with partners of group 5 (*other*) is 44.2% for males and 50.0% for females. Hence, the interactions with members of group 5 should not be ignored in the study of the effects of mixing patterns on the dynamics of sexually transmitted diseases.

To quantify the potential effect that individuals in group 5 may have on disease transmission, we need to estimate the elements of the last rows of the mixing matrix. The incomplete male and female mixing matrices are plotted in Figures 8 and 9, respectively. Despite the fact that these figures ignore the effects of group 5, they still show strong evidence of like-with-like mixing between members of the first four groups and a tendency for older males to interact with younger females. Obviously the usual assumption of random or proportionate mixing used in the mathematical modeling of STDs does not fit here.

To use the mark-recapture methodology, we assume that *sexually active* college students are

marked and *sexually active* individuals of group 5 are unmarked. The number of groups for males and females are the same, namely $I=J=5$. Our observers are the surveyed *sexually active* students. From equations in (18) we estimate the sizes of *sexually active* subgroups in group 5 of both genders:

$$\hat{T}_5^m = \frac{2377\ (136-68)}{68+1} = 2343 \quad \text{and} \quad \hat{T}_5^f = \frac{2304\ (120-67)}{67+1} = 1796.$$

Since K_5^m=1445.129 and K_5^f=1437.012, the lower bounds for the average number of partners for individuals in group 5 are

$$C_5^m \geq \max(1437.012/2343,\ 1) = \max(0.613,\ 1) = 1,$$

$$C_5^f \geq \max(1445.129/1796,\ 1) = \max(0.805,\ 1) = 1.$$

In addition, Equation (28) implies that

$$\tilde{C}_5^f = (2343/1796)\ \tilde{C}_5^m + (3331.09 - 2818.34)/1796 = 1.305\ \tilde{C}_5^m + 0.285 \geq \tilde{C}_5^m\ .$$

That is, the average number of partners per female in group 5 is greater than that for males, while the situation is reversed among individuals in groups 1, 2, and 4 (the values are very close in group 3). If we assume that $\tilde{C}_5^m$=1, then $\tilde{C}_5^f$=1.590; and from Equations (29) and (30) we obtain

$$\tilde{P}_{51}^m=0.086,\ \tilde{P}_{52}^m=0.062,\ \tilde{P}_{53}^m=0.194,\ \tilde{P}_{54}^m=0.056,\ \tilde{P}_{55}^m=0.683;$$

$$\tilde{P}_{51}^f=0.146,\ \tilde{P}_{52}^f=0.160,\ \tilde{P}_{53}^f=0.081,\ \tilde{P}_{54}^f=0.296,\ \tilde{P}_{55}^f=0.317.$$

Because of rounding, $\sum_{j=1}^{5} \tilde{P}_{5j}^m$ is not exactly equal to 1. The above calculation is used only to demonstrate the estimation procedure. Table 4 lists $\tilde{C}_5^f$, $\{\tilde{P}_{5j}^m\}$ and $\{\tilde{P}_{5i}^f\}$ calculated with double precision for different values of $\tilde{C}_5^m$. It is clear that $\tilde{C}_5^f$, $\tilde{P}_{55}^m$ and $\tilde{P}_{55}^f$ increase with $\tilde{C}_5^m$, while for other values of i and j, $\tilde{P}_{5j}^m$ and $\tilde{P}_{5i}^f$ decrease with $\tilde{C}_5^m$. Figures 10–13 illustrate the shape of the completed matrices with different values for the pair-formation parameter $\tilde{C}_5^m$. A second example that uses dating data from the same college population exhibits similar results (see (57)).

In this example, the data satisfy axioms (B1) and (B2) but not axiom (B3). The same is true for the estimated $\{\tilde{P}_{5j}^m\}$ and $\{\tilde{P}_{5i}^f\}$. Axiom (B3) is violated because we could not survey all individuals in the population.

8. Conclusions

Models for the dynamics of STD transmission have implicitly assumed that the mixing network is closed. Sociologists, epidemiologists, and theoreticians interested in connecting their models to data have not only found it difficult to collect these data but also have been forced by the modeling structure to construct data which assumes that the mixing network is closed. For example, some researchers have used racial data on marriages and assumed that the social/sexual mixing structure of a population is proportionally reflected in these data. This assumption not only imposes a like-with-like mixing structure but may also impose a like-with-like mixing structure that is independent of population dynamics such as preferred mixing. The danger of these assumptions may become more evident when we observe that the data presented here also took the existing superimposed social structure used in U.S. universities (first year, second year, etc.).

In this chapter, we have presented a mechanism for estimating the shape of a mixing matrix from a single survey. The data structure section helps identify the parameters needed for this estimation. We hope that this may be useful to researchers planning to construct survey instruments to identify the social structure of the population.

The role of non-target populations was highlighted because it played such a prominent role in our example. With data collected from a survey which asks specific questions about sexual behavior, the size of the *sexually active* non-target population can be conditionally estimated by using mark-recapture methodology. The condition is that all individuals in this *sexually active* non-target population have at least one sexual contact with individuals from the target population. We have also assumed that the average contact rates between target and non-target populations are similar--an assumption that could be relaxed if more data were available. Even after the estimation of the size of the *sexually active* non-target population was completed, one row was still missing in our mixing matrix for each gender. Point estimates of the elements of this row were carried out by assuming that the elements are consistent with the two-sex mixing axioms, which reduces the computation to that of estimating a single pair-formation parameter, namely the average number of partners for males (or females) in the non-target population. Lacking an independent estimate of this parameter left us no

alternative but that of declaring it a free parameter. The larger the free parameter, the larger the mixing proportion from the non-target population of a given gender to the non-target population of the other gender, and the smaller the corresponding mixing proportions to the target population.

The example of sexual behavior of college students reveals that the proportion of relationships with individuals from the non-target population is high (44.2% for males and 50.0% for females). Mixing matrices that exclude the non-target population may not provide a complete picture of the social network and may lead to erroneous conclusions. The example in Section 7 shows that random mixing is unlikely for this college population with the university's superimposed classification. There is some evidence of like-with-like preference and of pairing between older men and younger women within the groups in the target population.

If we use different criteria to categorize individuals, (*e.g.*, sexual activity), and consider members of the non-target population to be prostitutes, injecting drug users, or bisexuals, who may not be willing to respond to a survey and who may be at high risk of HIV/AIDS, what picture do we get? Long-term forecasting of HIV/AIDS is being carried out without estimates of the mixing matrices that model realistic, inconvenient social structures. Even the standard classifications used by the Centers for Disease Control lead to conclusions that may not hold up under a different classifying system. The fact that social and disease dynamics have not been systematically studied provides one more significant example of the importance of interdisciplinary research to better understand the spread of CD's.

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Table 1. Population sizes and sample sizes for males (upper line) and females (lower line)

Group	Population Size	Sample Size	Sexually Active Subsample Size	Sexually Active Proportion	Estimated Sexually Active Subpopulation Size
i/j	R	S	A	$A \div S$	$\hat{T}$
1	1673 1278	79 68	16 20	0.203 0.294	339 376
2	1589 1308	60 68	24 26	0.400 0.382	636 500
3	1591 1277	63 61	20 36	0.317 0.590	505 754
4	1686 1348	47 56	25 28	0.532 0.500	897 674
Total	6539 5211	249 253	85 110	0.341 0.435	2377 ($\hat{T}_+$) 2304

Table 2. Sexual partnership distribution of male students by counts ($U_{ij.}^{m}$, upper line) and proportions (P_{ij}^{m}, lower line)

Male	Female Partner Group j						Total	Average
Group	1	2	3	4	Subtotal	5		
i					X_i^m	(*Other*)	Y_i^m	C_i^m
1	12	3	1	1	17	10	27	1.69
	0.444	0.111	0.037	0.037		0.370		
2	2	9	2	2	15	17	32	1.33
	0.063	0.281	0.063	0.063		0.531		
3	0	4	4	4	12	14	26	1.30
	0.000	0.154	0.154	0.154		0.538		
4	1	4	7	11	23	12	35	1.40
	0.029	0.114	0.200	0.314		0.343		
Total	15	20	14	18	67(X_+^m)	53	120(Y_+^m)	1.41
	0.125	0.167	0.117	0.150		0.442		

Table 3. Sexual partnership distribution of female students by counts ($U^f_{ji\cdot}$, upper line) and proportions (P^f_{ji}, lower line)

Female	Male Partner Group i						Total	Average
Group	1	2	3	4	Subtotal	5		
j					X^f_j	(*Other*)	Y^f_j	C^f_j
1	5	3	4	3	15	14	29	1.45
	0.172	0.103	0.138	0.103		0.483		
2	1	13	5	2	21	15	36	1.38
	0.028	0.361	0.139	0.056		0.417		
3	2	4	11	7	24	18	42	1.17
	0.048	0.095	0.262	0.167		0.429		
4	0	0	1	7	8	21	29	1.04
	0.000	0.000	0.034	0.241		0.724		
Total	8	20	21	19	68(X^f_+)	68	136(Y^f_+)	1.24
	0.059	0.147	0.154	0.140		0.500		

Table 4. Mixing proportions of males ($\tilde{P}^m_{5j}$, upper line) and females ($\tilde{P}^f_{5i}$, lower line) in group 5 for different average numbers of partners ($\tilde{C}^m_5$)

		$\tilde{P}^m_{5j}$ (upper line) or $\tilde{P}^f_{5i}$ (lower line)				
		j or i				
$\tilde{C}^m_5$	$\tilde{C}^f_5$	1	2	3	4	5
1.000	1.592	0.086 0.146	0.062 0.160	0.193 0.081	0.055 0.296	0.603 0.318
1.500	2.245	0.057 0.103	0.041 0.114	0.129 0.057	0.036 0.210	0.736 0.516
2.000	2.897	0.043 0.080	0.031 0.088	0.097 0.044	0.027 0.163	0.802 0.625
2.500	3.549	0.034 0.065	0.025 0.072	0.077 0.036	0.022 0.133	0.841 0.694
3.000	4.202	0.029 0.055	0.021 0.061	0.064 0.031	0.018 0.112	0.868 0.741
3.500	4.854	0.025 0.048	0.018 0.053	0.055 0.026	0.016 0.097	0.887 0.776

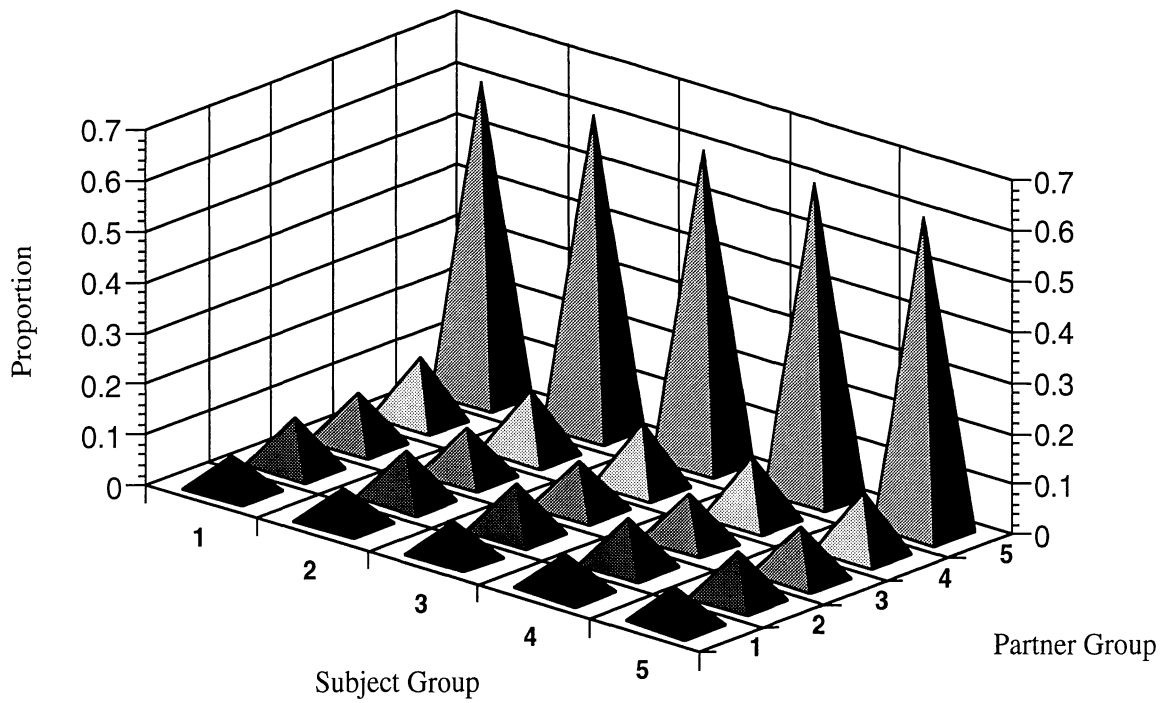

Fig. 1 Example graph of one-sex random mixing

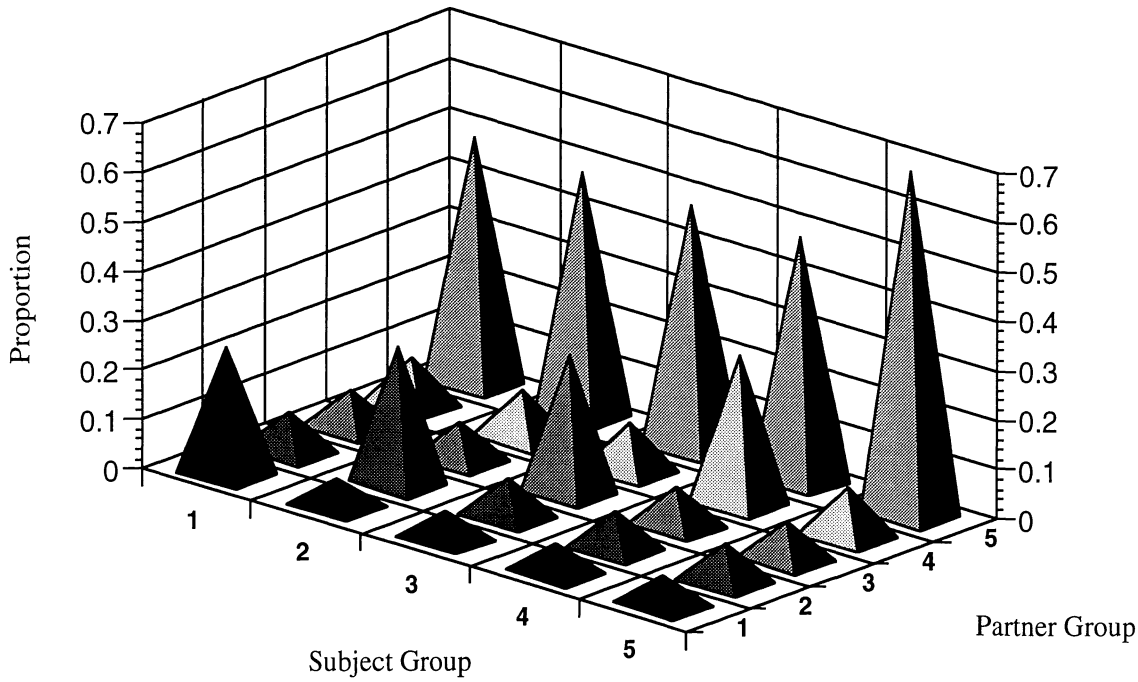

Fig. 2 Example graph 1 of one-sex preferred mixing

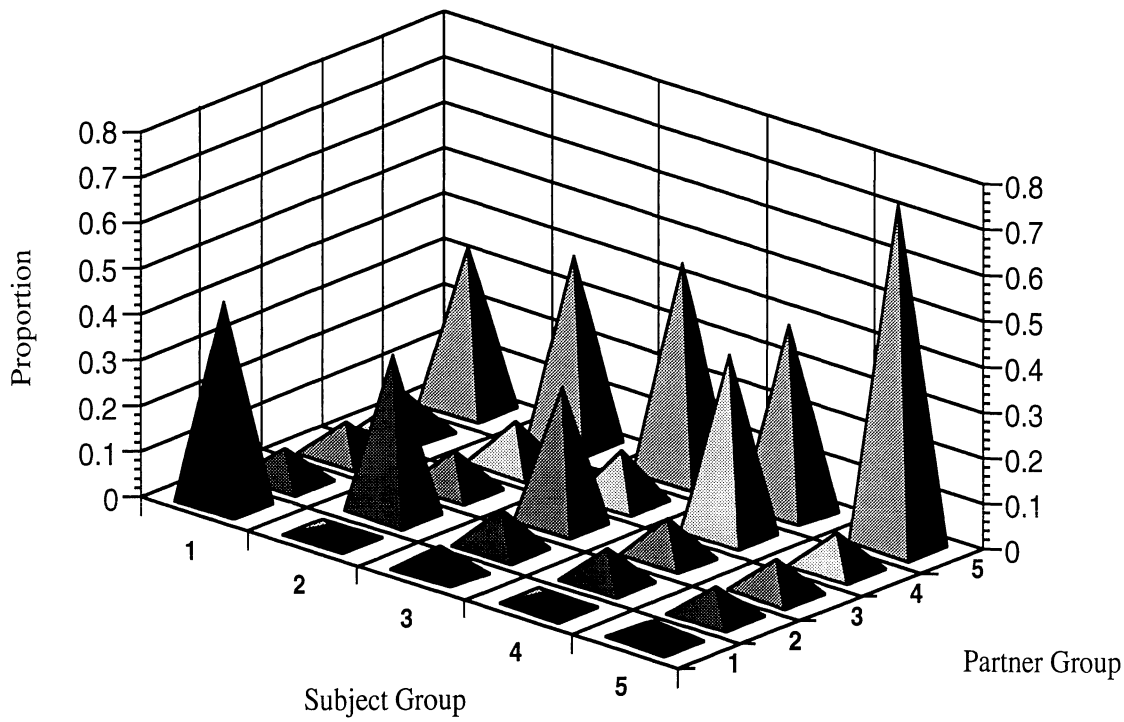

Fig. 3 Example graph 2 of one-sex preferred mixing

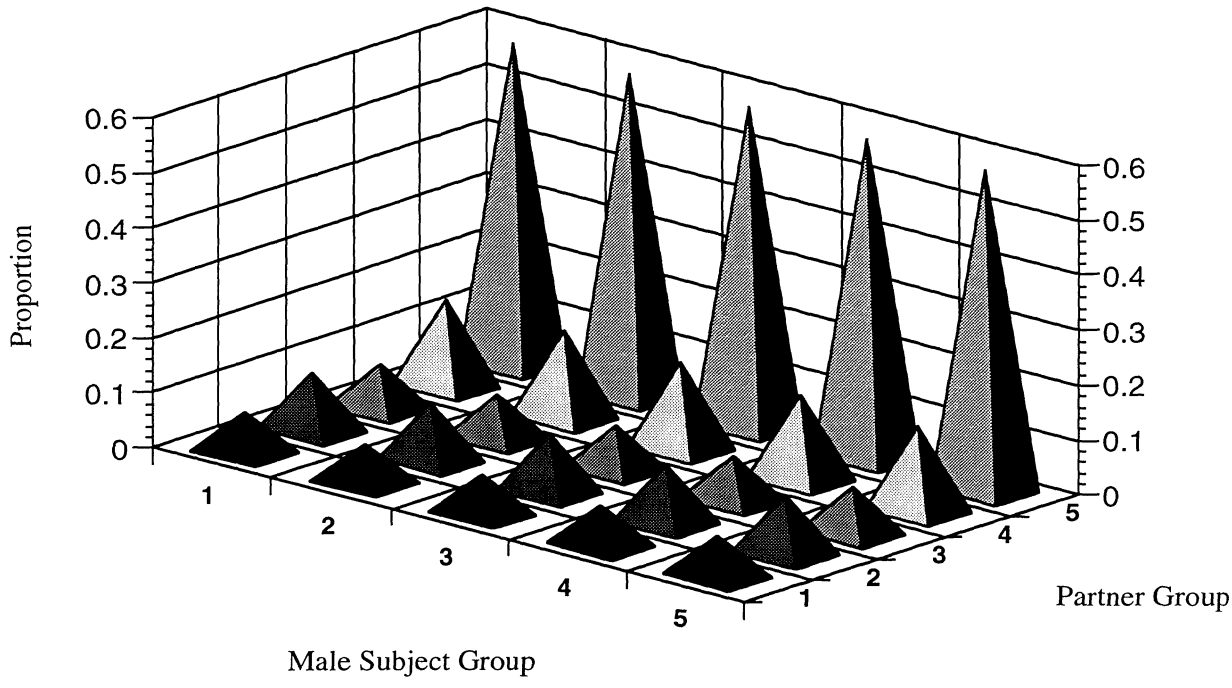

Fig. 4 Example graph of two-sex random mixing for males

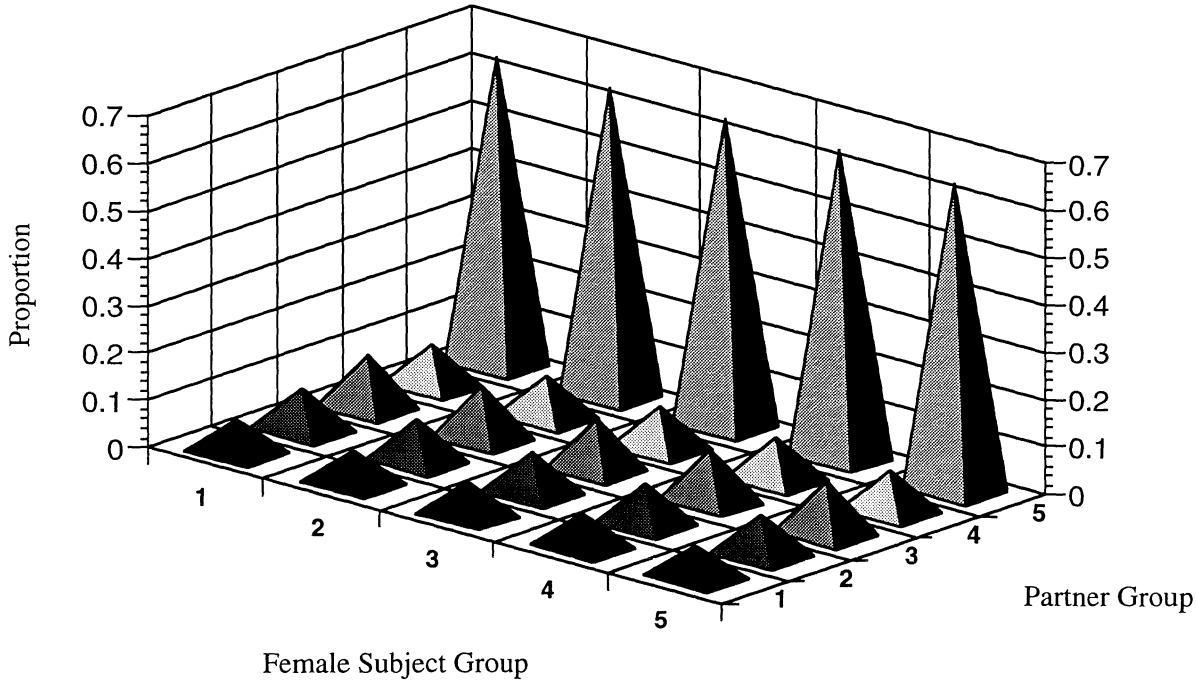

Fig. 5 Example graph of two-sex random mixing for females

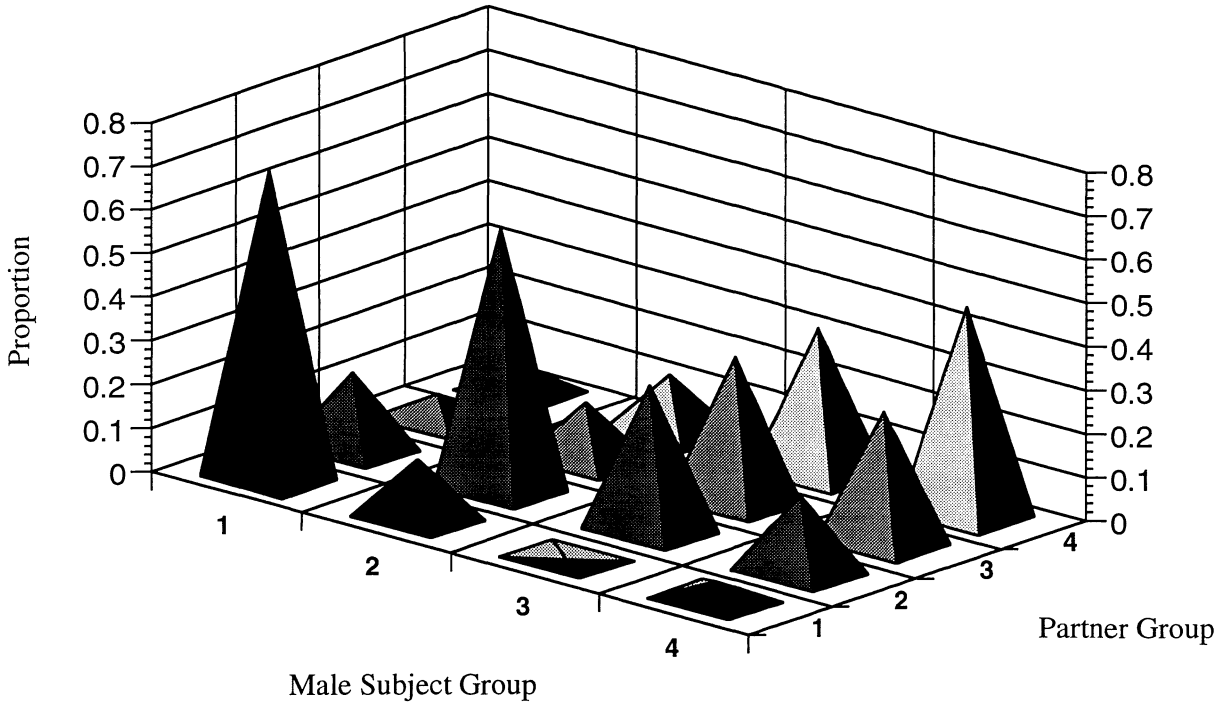

Fig. 6 Example graph of two-sex mixing for males

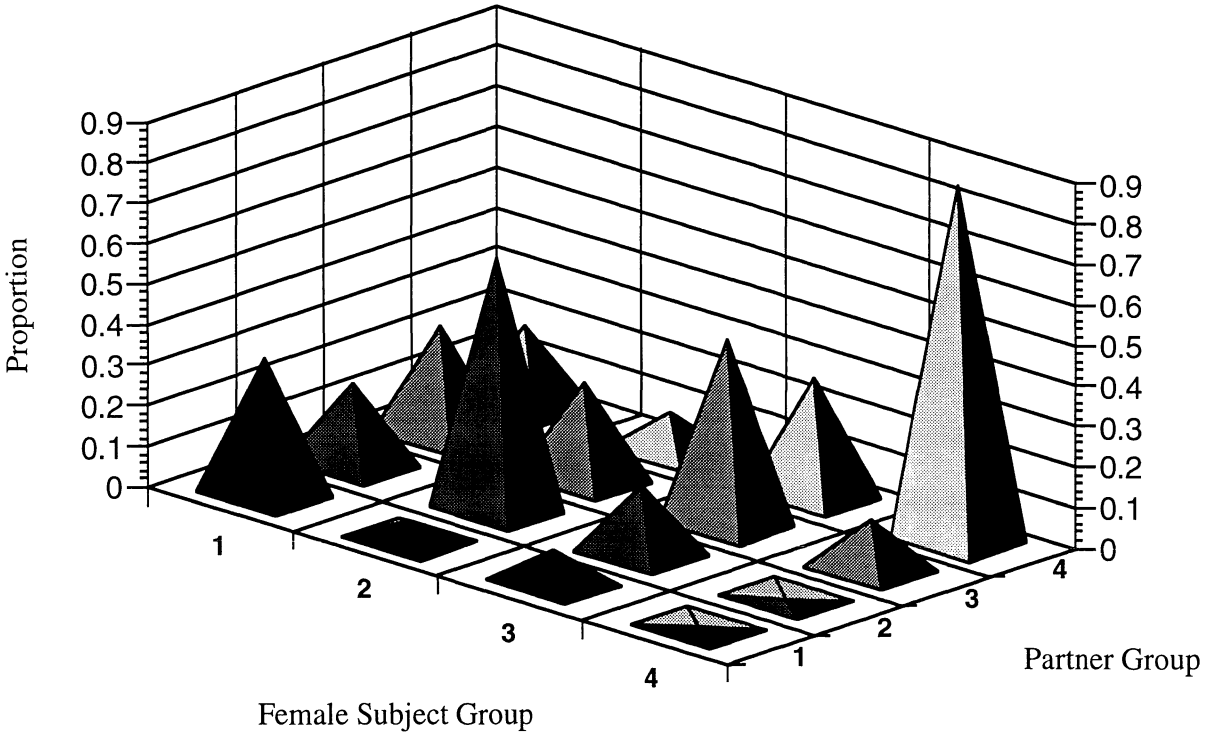

Fig. 7 Example graph of two-sex mixing for females

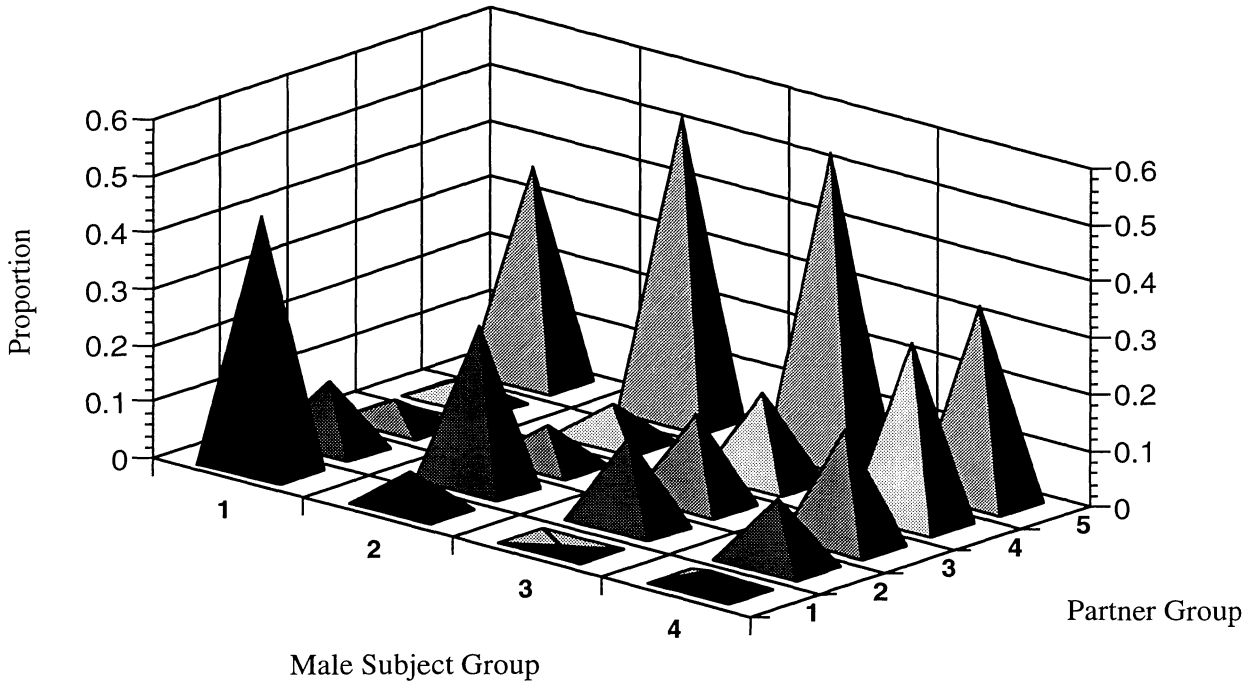

Fig. 8 Male incomplete mixing matrix from data

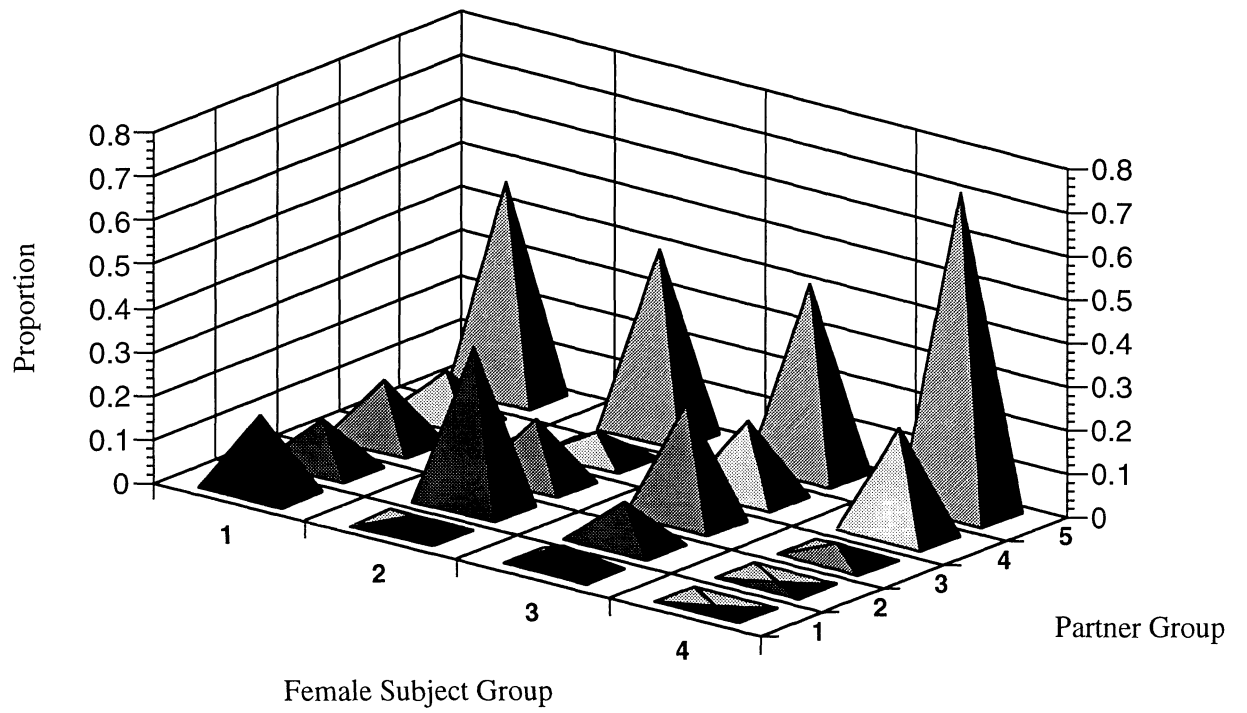

Fig. 9 Female incomplete mixing matrix from data

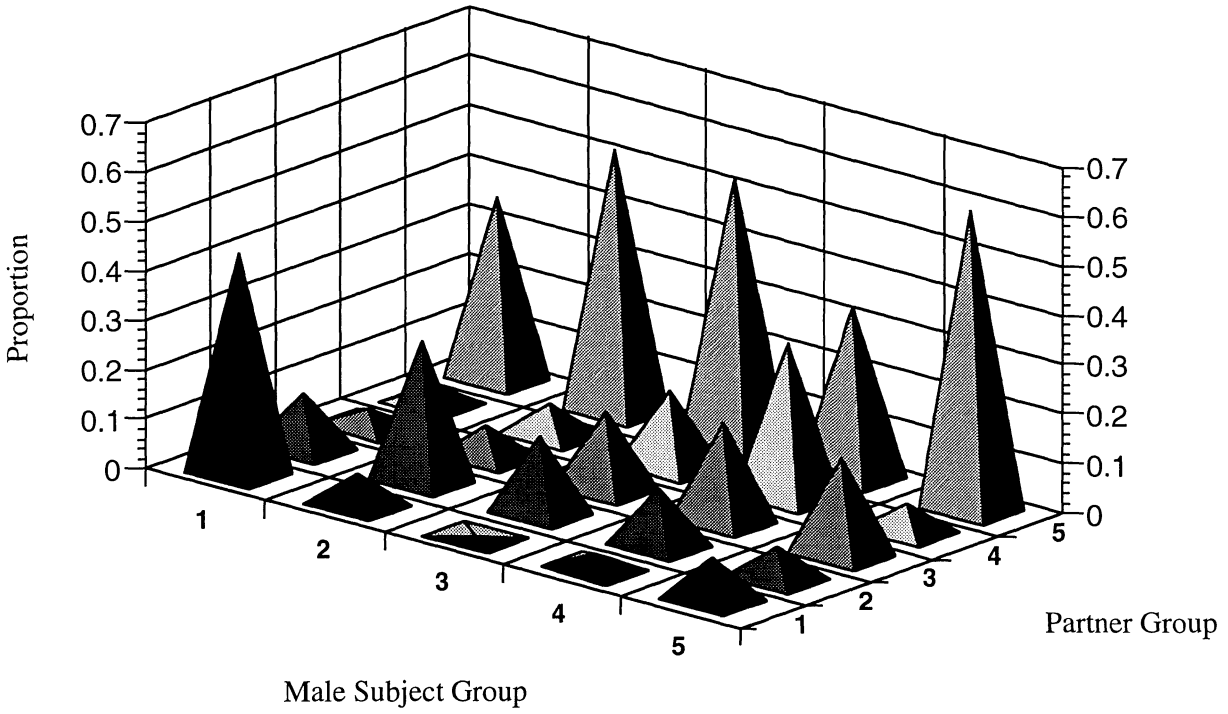

Fig. 10 Completed male mixing matrix from data with pair-formation parameter=1

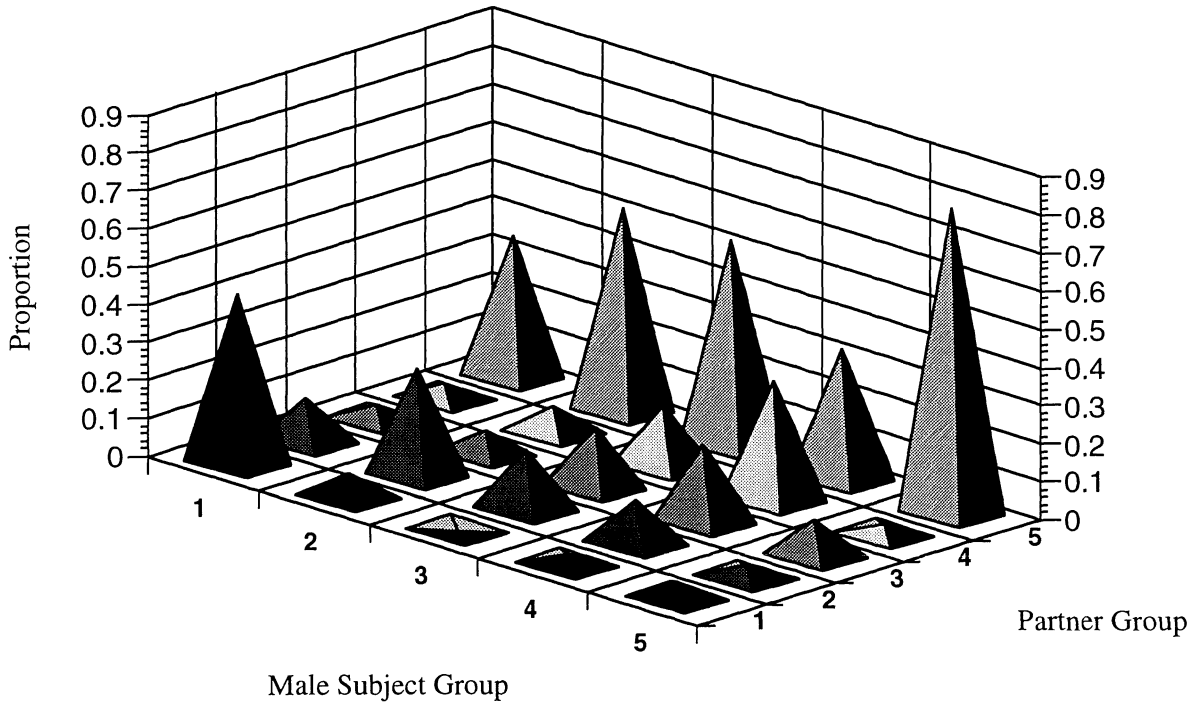

Fig. 11 Completed male mixing matrix from data with pair-formation parameter=2

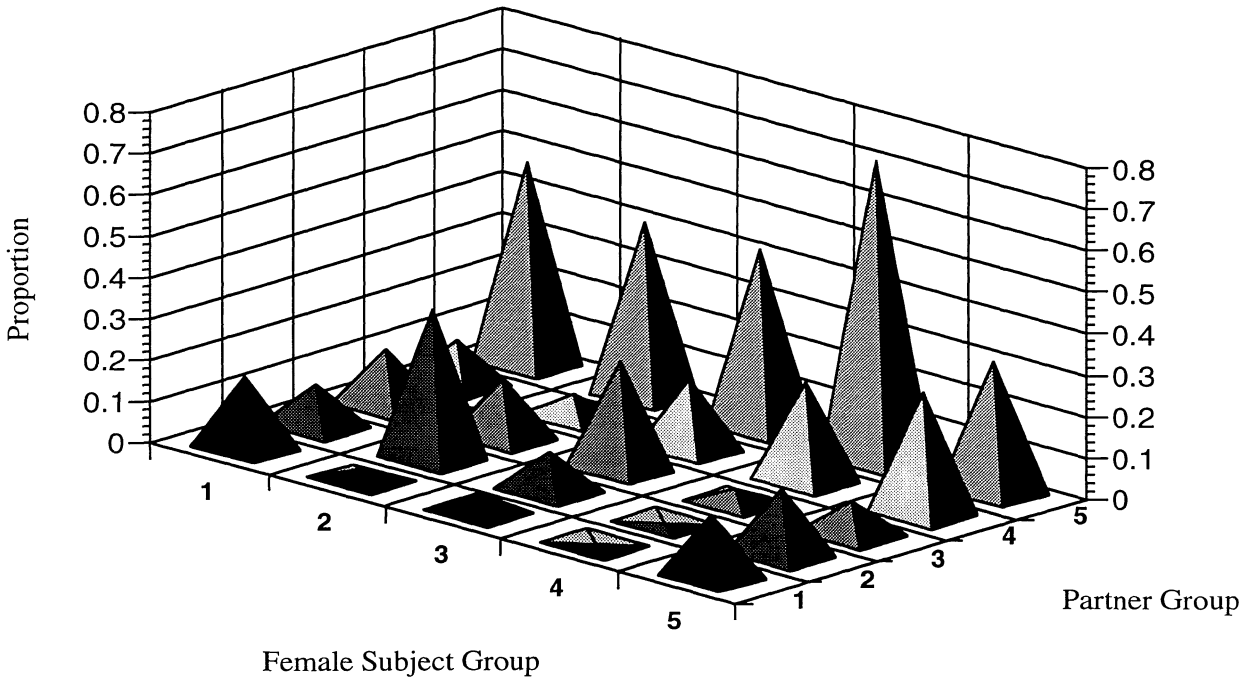

Fig. 12 Completed female mixing matrix from data with pair-formation parameter=1

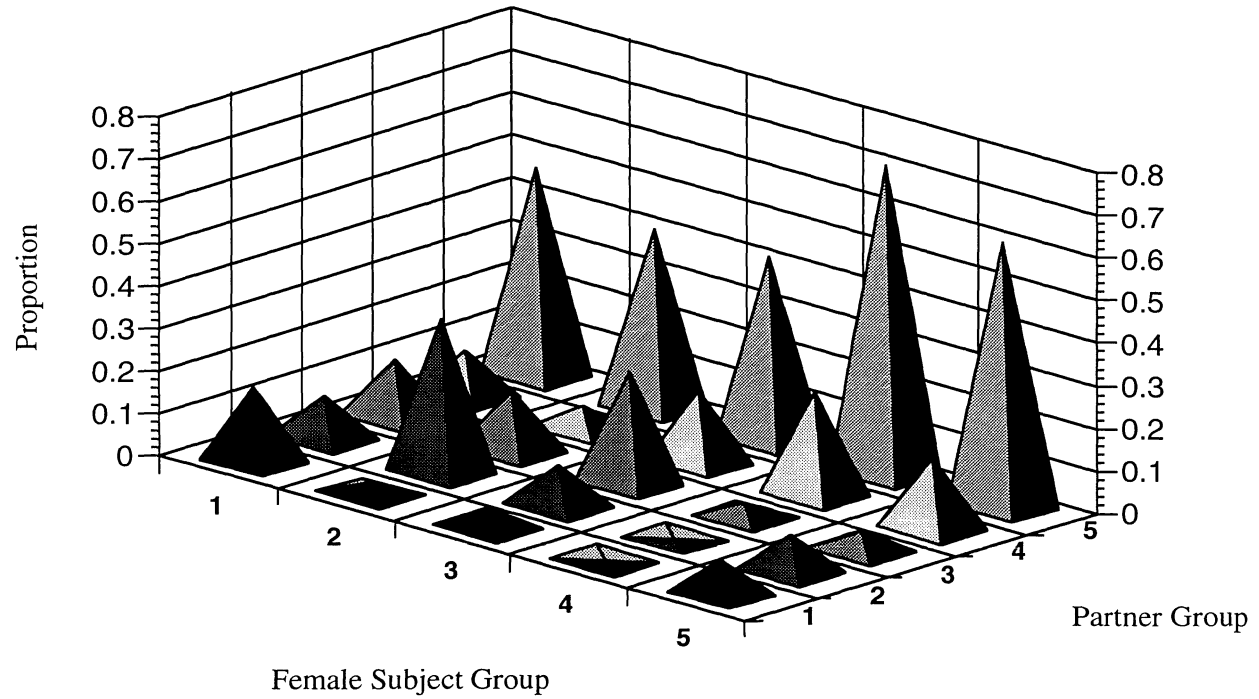

Fig. 13 Completed female mixing matrix from data with pair-formation parameter=2